ABSTRACT

Method for identifying biological species

The present invention provides a method for identifying species and subspecies in a biological sample through the selective amplification of segments of nucleic acid that code a target region of the cytoplasmatic beta-actin protein, which is present in all the organisms concerned. The method comprises DNA extraction from the sample; amplification of divergent segments of the cytoplasmatic beta-actin gene by PCR or an equivalent technique, using primers of regions with high evolutionary conservation between species and subspecies; and identification of the amplified segment by comparison of its size in base pairs with a pre-established standard of sizes and/or identification of the amplified segment by DNA sequencing and comparison of the resulting sequence with the specific sequence of each species or subspecies present on a computer database.